

GenCore version 5.1.4-p5.4578
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OM protein - protein search, using sw model

Run on: May 11, 2003, 02:05:38 ; Search time 37 Seconds
(without alignments)
280.609 Million cell updates/sec

Title: US-09-914-324A-1

Perfect score: 616
Sequence: 1 MAAMADVDPSTGNSGAGK.....KTRQVCPDLDNREMEFQKYGH 108

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR_73:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	616	100.0	108	T51146	ring-box protein 1
2	510	82.8	136	T13388	hypothetical prote
3	499	81.0	115	T47341	ring-box protein-1
4	493	80.0	110	T27823	hypothetical prote
5	469	76.1	107	T38310	pop-interacting pr
6	385	62.5	121	S66830	hypothetical prote
7	378	61.4	166	T18513	hypothetical prote
8	266	43.2	112	T29620	hypothetical prote
9	164.5	26.7	94	T38652	hypothetical prote
10	146.5	23.8	135	T21802	hypothetical prote
11	136	22.1	165	S52511	hypothetical prote
12	132.5	21.5	99	G90113	Rbpl protein [limo
13	116.5	18.9	2160	T20241	hypothetical prote
14	104	16.9	349	T06680	hypothetical prote
15	102.5	16.6	249	C96775	hypothetical prote
16	102	16.6	210	T16534	zinc-finger-like p
17	100	16.2	676	T47637	hypothetical prote
18	97	15.7	159	T48209	hypothetical prote
19	97	15.7	327	D86474	probable RING zinc
20	96	15.6	332	E86448	hypothetical prote
21	95.5	15.5	441	E71425	hypothetical prote
22	95	15.4	253	T06113	hypothetical prote
23	95	15.4	322	H85474	hypothetical prote
24	95	15.4	336	T28358	ORF MSV197 tryptop
25	95	15.4	362	T51464	RING-H2 zinc finger
26	95	15.4	530	T50499	hypothetical prote
27	95	15.4	689	E84811	probable retroelem
28	92	14.9	185	T51844	RING-H2 finger pro
29	91.5	14.9	190	T51859	RING-H2 finger pro

30	91.5	14.9	496	B96674	hypothetical prote
31	91.5	14.9	571	T40911	probable PHD-type
32	91	14.8	530	T28366	ORF MSV205 tryptop
33	90.5	14.7	677	T39713	zinc finger protei
34	90	14.6	213	T14811	hypothetical prote
35	90	14.6	532	T49467	related to COP1-in
36	90	14.5	1208	T05077	hypothetical prote
37	89.5	14.5	202	T06621	hypothetical prote
38	89.5	14.5	624	T01585	probable RING zinc
39	89	14.4	357	E85092	hypothetical prote
40	89	14.4	456	T19377	hypothetical prote
41	88.5	14.4	336	A86406	probable RING zinc
42	88.5	14.4	524	F96572	protein R12M16.10
43	88	14.3	141	S15788	intermediate early
44	88	14.3	161	E88541	protein ZK637.14 [
45	88	14.3	200	T41745	RING-H2 finger pro

ALIGNMENTS

RESULT 1

T51146

ring-box protein 1 [imported] - human

C.Species: Homo sapiens (man)

C.Date: 28-Jul-2000 #sequence_revision 28-Jul-2000 #text_change 28-Jul-2000

C.Accession: T51146

R.Kamura, T.; Keop, D.M.; Conrad, M.N.; Skowyra, D.; Moreland, R.J.; Iliopoulos, O.;

Science 284, 657-661, 1999

A.Title: Rbx1, a component of the VHL tumor suppressor complex and SCF ubiquitin ligase

A.Reference number: 225317; PMID:99234320; PMID:10213691

A.Accession: T51146

A.Status: preliminary; translated from GB/EMBL/DBJ

A.Molecule type: mRNA

A.Residues: 1-108 <KAM>

A.Cross-references: EMBL:AF140598; PIDN:AAD29715.1

C.Genetics:

A.Gene: RBX1

Query Match

Best local similarity 100.0%; Score 616; DB 2; Length 108;

Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAMADVDPSTGNSGAGKREVKKNVAVLWAMDIYVNDCAICRNHIMDCIEQANQ 60

DB 1 MAAMADVDPSTGNSGAGKREVKKNVAVLWAMDIYVNDCAICRNHIMDCIEQANQ 60

QY 61 ASATSECTVAMGVCNHAFFHCISRMLKTRQVCPDLDNREMEFQKYGH 108

DB 61 ASATSECTVAMGVCNHAFFHCISRMLKTRQVCPDLDNREMEFQKYGH 108

RESULT 2

T13388

hypothetical protein 11502.11 - fruit fly (Drosophila melanogaster)

C.Species: Drosophila melanogaster

C.Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000

R.Salles, C.; Valenti, P.; Darlamiou, A.; Henderson, N.; Campbell, L.; Glover, D.

submitted to the EMBL Data Library, May 1999

A.Description: Sequencing the distal X chromosome of Drosophila melanogaster.

A.Reference number: 217665

A.Accession: T13388

A.Status: preliminary; translated from GB/EMBL/DBJ

A.Molecule type: DNA

A.Residues: 1-136 <CAT>

A.Cross-references: EMBL:AL031581; PIDN:CAA20888.1

C.Genetics:

A.Cross-references: FlyBase:FBgn0020381

A.Introns: 64/1

A.Note: EG:11502.11

Query Match

82.8%; Score 510; DB 2; Length 136;

Best Local Similarity 69.3%, Pred. No. 4e-47;
Matches 95; Conservative 4; Mismatches 4; Indels 34; Gaps 3;

QY 5 MDVD-----TPSGTNSGAGKRRFEVYK-----WNAVA 31
| : : : : :
Db 1 MEVEDGEYEVSSSSKSG-DKKRFYKVSQOOSKRVIVNECTDGTSSFPLRRQMNVA 59
QY 32 LMAMDIVVNCALICRNHIMDLCEIQANQASATSECTVAMGVCNHAHFHCISRWLTKR 91
| : : : : :
Db 60 LMAMDIVVNCALICRNHIMDLCEIQANQASATSECTVAMGVCNHAHFHCISRWLTKR 119
QY 92 QVCPDLNREMEFQRYGH 108
| : : : : :
Db 120 QVCPDLNREMEFQRYGH 136

RESULT 3
T47341

ring-box protein-like - Arabidopsis thaliana

N:Alternate names: protein T21C14.50

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 02-Aug-2002

C:Accession: T47341

R:Deiseny, M.; Berger, C.; Cooke, R.; Gaubier, P.; Grellet, F.; Laudie, M.; Mewes, H.W.;

submitted to the Protein Sequence Database, April 2000

A:Reference number: Z24462

A:Accession: T47341

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-115

A:Cross-references: EMBL:AL138639

A:Experimental source: cultivar Columbia; BAC clone T21C14

C:Genetics:

A:Map position: 3

A:Introns: 43/71; 60/1; 104/1

A:Note: T21C14.50

C:Superfamily: yeast hypothetical protein YOL133w; RING finger homology

Query Match

Best Local Similarity 81.0%; Score 499; DB 2; Length 115;
Matches 88; Conservative 5; Mismatches 13; Indels 2; Gaps 1;

QY 1 MAAMDVTPSGTNSGAGKRRFEVYKKNVAVALMAMDIVVNCALICRNHIMDLCEIQANQ 60
| : : : : :
Db 10 MESSSSISVPS--SSSKSKRFELKMSAVALLMAMDIVVNCALICRNHIMDLCEIQANQ 67

RESULT 4
T27823

hypothetical protein ZK287.5 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T27823

R:McMurray, A. submitted to the EMBL Data Library, April 1996

A:Accession: T27823

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-110 <WILL>

A:Cross-references: EMBL:Z70757; PIDN:CAA94801.1; GSPDB:GN00023; CESP:ZK287.5

A:Experimental source: clone ZK287

C:Genetics:

A:Gene: CESP:ZK287.5

A:Map position: 5

A:Introns: 25/3; 94/3

Query Match 80.0%; Score 493; DB 2; Length 110;

Best Local Similarity 79.3%, Pred. No. 2.1e-45;
Matches 88; Conservative 5; Mismatches 14; Indels 4; Gaps 2;

QY 1 MAAMD---VTPSGTNSGAGKRRFEVYKKNVAVALMAMDIVVNCALICRNHIMDLCEIQ 57
| : : : : :
Db 1 MAQASDSTAMEYEATNTQTV-KKRFYKMSAVALLMAMDIVVNCALICRNHIMDLCEIQ 59
QY 58 ANQASATSECTVAMGVCNHAHFHCISRWLTKRQVCPDLNREMEFQRYGH 108
| : : : : :
Db 60 ANQAGLDECTVAMGVCNHAHFHCISRWLTKRQVCPDLNREMEFQRYGH 110

RESULT 5
T38310

pop-interacting protein 1 - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe

C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999

C:Accession: T38310

R:Brown, D.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V. submitted to the EMBL Data Library, September 1997

A:Reference number: Z21733

A:Accession: T38310

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-107 <BRQ>

A:Cross-references: EMBL:Z98977; PIDN:CA58559.1; GSPDB:GN00066; SPDB:SPAC23H4.18c

A:Experimental source: strain 972h-; cosmid c23H4

C:Genetics:

A:Gene: SPDB:SPAC23H4.18c

A:Map position: 1

A:Introns: 25/3; 75/3; 106/1

Query Match

Best Local Similarity 76.1%; Score 469; DB 2; Length 107;
Matches 77; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 21 RFEYKKNVAVALMAMDIVVNCALICRNHIMDLCEIQANQASATSECTVAMGVCNHAHF 80
| : : : : :
Db 20 RFEIKKNVAVALMAMDIVVNCALICRNHIMDLCEIQANQASATSECTVAMGVCNHAHF 79

RESULT 6
S66830

hypothetical protein YOL133w - yeast (Saccharomyces cerevisiae)

N:Alternate names: hypothetical protein AOA121; hypothetical protein 00511

C:Species: Saccharomyces cerevisiae

C>Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 02-Aug-2002

C:Accession: S66830; S72035

R:Ariño, J.; Casamayor, A.; Gano, F.J.; Gancedo, C.; Lafuente, M.J.; Aldea, M.; Casas submitted to the Protein Sequence Database, July 1996

A:Reference number: S66814

A:Accession: S66830

A:Molecule type: DNA

A:Residues: 1-121 <ARI>

A:Cross-references: EMBL:Z74876; NID:91420022; PID:91420024; MIPS:YOL133w

A:Experimental source: strain S288c

R:Aldea, M.; Piedrafitá, L.; Casas, C.; Casamayor, A.; Khalid, H.; Balcells, L.; Arin yeast 12, 1053-1058, 1996

A>Title: Sequence analysis of a 12 801 bp fragment of the left arm of yeast chromosome protein and six other open reading frames.

A:Reference number: S72030; MUID:97051593; PMID:8896270

A:Accession: S72035

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-121 <ALD>

A:Cross-references: EMBL:X95465; NID:91628437; PIDN:CAA6473.1; PID:91628443

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, DNA

C:Genetics:

A:Gene: SGD:HRT1

